CLAIMS

1. An aspartokinase variant having at least 80% sequence identity to SEQ ID NO: 1 having aspartokinase activity, wherein the amino acid at position 377 in the amino acid sequence of SEQ ID NO: 1 is substituted with L-lysine or L-methionine.

2. A polynucleotide encoding the variant of claim 1.

3. A microorganism of the genus *Corynebacterium*, which produces an aspartate-derived L-amino acid or an amino acid derivative thereof comprising the aspartokinase variant of claim 1, wherein the aspartate-derived L-amino acid or amino acid derivative thereof is selected from the group consisting of lysine, threonine, methionine, homoserine, O-acetylhomoserine, O-succinylhomoserine, isoleucine, and cadaverine.

4. The microorganism according to claim 3, wherein the microorganism of the genus *Corynebacterium* is *Corynebacterium glutamicum*.

5. A method for producing an aspartate-derived L-amino acid or an amino acid derivative thereof, comprising:

culturing the microorganism of claim 3 in a medium; and

recovering the aspartate-derived L-amino acid or amino acid derivative thereof from the cultured microorganism or cultured medium, wherein the aspartate-derived L-amino acid or amino acid derivative thereof is selected from the group consisting of lysine, threonine, methionine, homoserine, O-acetylhomoserine, O-succinylhomoserine, isoleucine, and cadaverine.

6. The method according to claim 5, wherein the microorganism of the genus *Corynebacterium* is *Corynebacterium glutamicum*.

7. A method for producing L-methionine, comprising:

culturing the microorganism of claim 3 in a medium;

producing *O*-acetylhomoserine or *O*-succinylhomoserine from the cultured microorganism or cultured medium; and

converting the *O*-acetylhomoserine or *O*-succinylhomoserine to L-methionine.

8. The method according to claim 7, wherein the microorganism of the genus *Corynebacterium* is *Corynebacterium glutamicum*.